



PCT

RAW SEQUENCE LISTING

DATE: 07/14/2004

PATENT APPLICATION: US/10/500,665

TIME: 09:35:01

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07142004\J500665.raw

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3 <110> APPLICANT: Leone, Arturo
4     Turco, Maria Caterina
6 <120> TITLE OF INVENTION: BAG3 nucleotide and protein sequences to be used in
research, diagnostics
7     and therapy for cell death-involving diseases
9 <130> FILE REFERENCE: 3135PT nat'l phases
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/500,665
C--> 12 <141> CURRENT FILING DATE: 2004-06-28
14 <150> PRIOR APPLICATION NUMBER: EP01830834.6
15 <151> PRIOR FILING DATE: 2001-12-28
17 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2533
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (307)..(2034)
29 <223> OTHER INFORMATION: Human BAG3 gene sequence
30     NCBI Pub Med Accession Number: XM_055575
31     Homo sapiens BCL2-associated athanogene 3 (BAG3)
34 <400> SEQUENCE: 1
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37 ctagccggcc agttgctacc tccctttatc tctctcttcc cctctggcag cgaggaggct      120
39 atttccagac acttccaccc ctctctggcc acgtcacccc cgctttaa tcataaaggt      180
41 gcccggcgcc ggcttcccgg acacgtcggc ggcggagagg ggcccacggc ggcggcccgg      240
43 ccagagactc ggcgcccggg gccagcgcgc cgcacccgcg cccagcggg cagaccccaa      300
45 cccagc atg agc gcc gcc acc cac tcg ccc atg atg cag gtg gcg tcc      348
46     Met Ser Ala Ala Thr His Ser Pro Met Met Gln Val Ala Ser
47     1             5             10
49 ggc aac ggt gac cgc gac cct ttg ccc ccc gga tgg gag atc aag atc      396
50 Gly Asn Gly Asp Arg Asp Pro Leu Pro Pro Gly Trp Glu Ile Lys Ile
51 15             20             25             30
53 gac ccg cag acc ggc tgg ccc ttc ttc gtg gac cac aac agc cgc acc      444
54 Asp Pro Gln Thr Gly Trp Pro Phe Phe Val Asp His Asn Ser Arg Thr
55             35             40             45
57 act acg tgg aac gac ccg cgc gtg ccc tct gag ggc ccc aag gag act      492
58 Thr Thr Trp Asn Asp Pro Arg Val Pro Ser Glu Gly Pro Lys Glu Thr
59             50             55             60
61 cca tcc tct gcc aat ggc cct tcc cgg gag ggc tct agg ctg ccg cct      540
62 Pro Ser Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser Arg Leu Pro Pro
63             65             70             75
65 gct agg gaa ggc cac cct gtg tac ccc cag ctc cga cca ggc tac att      588

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66 Ala Arg Glu Gly His Pro Val Tyr Pro Gln Leu Arg Pro Gly Tyr Ile
67      80                      85                      90
69 ccc att cct gtg ctc cat gaa ggc gct gag aac cgg cag gtg cac cct      636
70 Pro Ile Pro Val Leu His Glu Gly Ala Glu Asn Arg Gln Val His Pro
71 95                      100                      105                      110
73 ttc cat gtc tat ccc cag cct ggg atg cag cga ttc cga act gag gcg      684
74 Phe His Val Tyr Pro Gln Pro Gly Met Gln Arg Phe Arg Thr Glu Ala
75                      115                      120                      125
77 gca gca gcg gct cct cag agg tcc cag tca cct ctg cgg ggc atg cca      732
78 Ala Ala Ala Ala Pro Gln Arg Ser Gln Ser Pro Leu Arg Gly Met Pro
79                      130                      135                      140
81 gaa acc act cag cca gat aaa cag tgt gga cag gtg gca gcg gcg gcg      780
82 Glu Thr Thr Gln Pro Asp Lys Gln Cys Gly Gln Val Ala Ala Ala Ala
83                      145                      150                      155
85 gca gcc cag ccc cca gcc tcc cac gga cct gag cgg tcc cag tct cca      828
86 Ala Ala Gln Pro Pro Ala Ser His Gly Pro Glu Arg Ser Gln Ser Pro
87                      160                      165                      170
89 gct gcc tct gac tgc tca tcc tca tcc tcc tcg gcc agc ctg cct tcc      876
90 Ala Ala Ser Asp Cys Ser Ser Ser Ser Ser Ala Ser Leu Pro Ser
91 175                      180                      185                      190
93 tcc ggc agg agc agc ctg ggc agt cac cag ctc ccg cgg ggg tac atc      924
94 Ser Gly Arg Ser Ser Leu Gly Ser His Gln Leu Pro Arg Gly Tyr Ile
95                      195                      200                      205
97 tcc att ccg gtg ata cac gag cag aac gtt acc cgg cca gca gcc cag      972
98 Ser Ile Pro Val Ile His Glu Gln Asn Val Thr Arg Pro Ala Ala Gln
99                      210                      215                      220
101 ccc tcc ttc cac caa gcc cag aag acg cac tac cca gcg cag cag ggg      1020
102 Pro Ser Phe His Gln Ala Gln Lys Thr His Tyr Pro Ala Gln Gln Gly
103                      225                      230                      235
105 gag tac cag acc cac cag cct gtg tac cac aag atc cag ggg gat gac      1068
106 Glu Tyr Gln Thr His Gln Pro Val Tyr His Lys Ile Gln Gly Asp Asp
107                      240                      245                      250
109 tgg gag ccc cgg ccc ctg cgg gcg gca tcc ccg ttc agg tca tct gtc      1116
110 Trp Glu Pro Arg Pro Leu Arg Ala Ala Ser Pro Phe Arg Ser Ser Val
111 255                      260                      265                      270
113 cag ggt gca tcg agc cgg gag ggc tca cca gcc agg agc agc acg cca      1164
114 Gln Gly Ala Ser Ser Arg Glu Gly Ser Pro Ala Arg Ser Ser Thr Pro
115                      275                      280                      285
117 ctc cac tcc ccc tcg ccc atc cgt gtg cac acc gtg gtc gac agg cct      1212
118 Leu His Ser Pro Ser Pro Ile Arg Val His Thr Val Val Asp Arg Pro
119                      290                      295                      300
121 cag cag ccc atg acc cat cga gaa act gca cct gtt tcc cag cct gaa      1260
122 Gln Gln Pro Met Thr His Arg Glu Thr Ala Pro Val Ser Gln Pro Glu
123                      305                      310                      315
125 aac aaa cca gaa agt aag cca ggc cca gtt gga cca gaa ctc cct cct      1308
126 Asn Lys Pro Glu Ser Lys Pro Gly Pro Val Gly Pro Glu Leu Pro Pro
127                      320                      325                      330
129 gga cac atc cca att caa gtg atc cgc aaa gag gtg gat tct aaa cct      1356
130 Gly His Ile Pro Ile Gln Val Ile Arg Lys Glu Val Asp Ser Lys Pro

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131	335	340	345	350	
133	gtt tcc cag aag ccc cca cct ccc tct gag aag gta gag gtg aaa gtt	1404			
134	Val Ser Gln Lys Pro Pro Pro Pro Ser Glu Lys Val Glu Val Lys Val				
135	355	360	365		
137	ccc cct gct cca gtt cct tgt cct cct ccc agc cct ggc cct tct gct	1452			
138	Pro Pro Ala Pro Val Pro Cys Pro Pro Pro Ser Pro Gly Pro Ser Ala				
139	370	375	380		
141	gtc ccc tct tcc ccc aag agt gtg gct aca gaa gag agg gca gcc ccc	1500			
142	Val Pro Ser Ser Pro Lys Ser Val Ala Thr Glu Glu Arg Ala Ala Pro				
143	385	390	395		
145	agc act gcc cct gca gaa gct aca cct cca aaa cca gga gaa gcc gag	1548			
146	Ser Thr Ala Pro Ala Glu Ala Thr Pro Pro Lys Pro Gly Glu Ala Glu				
147	400	405	410		
149	gct ccc cca aaa cat cca gga gtg ctg aaa gtg gaa gcc atc ctg gag	1596			
150	Ala Pro Pro Lys His Pro Gly Val Leu Lys Val Glu Ala Ile Leu Glu				
151	415	420	425	430	
153	aag gtg cag ggg ctg gag cag gct gta gac aac ttt gaa ggc aag aag	1644			
154	Lys Val Gln Gly Leu Glu Gln Ala Val Asp Asn Phe Glu Gly Lys Lys				
155	435	440	445		
157	act gac aaa aag tac ctg atg atc gaa gag tat ttg acc aaa gag ctg	1692			
158	Thr Asp Lys Lys Tyr Leu Met Ile Glu Glu Tyr Leu Thr Lys Glu Leu				
159	450	455	460		
161	ctg gcc ctg gat tca gtg gac ccc gag gga cga gcc gat gtg cgt cag	1740			
162	Leu Ala Leu Asp Ser Val Asp Pro Glu Gly Arg Ala Asp Val Arg Gln				
163	465	470	475		
165	gcc agg aga gac ggt gtc agg aag gtt cag acc atc ttg gaa aaa ctt	1788			
166	Ala Arg Arg Asp Gly Val Arg Lys Val Gln Thr Ile Leu Glu Lys Leu				
167	480	485	490		
169	gaa cag aaa gcc att gat gtc cca ggt caa gtc cag gtc tat gaa ctc	1836			
170	Glu Gln Lys Ala Ile Asp Val Pro Gly Gln Val Gln Val Tyr Glu Leu				
171	495	500	505	510	
173	cag ccc agc aac ctt gaa gca gat cag cca ctg cag gca atc atg gag	1884			
174	Gln Pro Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln Ala Ile Met Glu				
175	515	520	525		
177	atg ggt gcc gtg gca gca gac aag ggc aag aaa aat gct gga aat gca	1932			
178	Met Gly Ala Val Ala Ala Asp Lys Gly Lys Lys Asn Ala Gly Asn Ala				
179	530	535	540		
181	gaa gat ccc cac aca gaa acc cag cag cca gaa gcc aca gca gca gcg	1980			
182	Glu Asp Pro His Thr Glu Thr Gln Gln Pro Glu Ala Thr Ala Ala Ala				
183	545	550	555		
185	act tca aac ccc agc agc atg aca gac acc cct ggt aac cca gca gca	2028			
186	Thr Ser Asn Pro Ser Ser Met Thr Asp Thr Pro Gly Asn Pro Ala Ala				
187	560	565	570		
189	ccg tag cctctgccct gtaaaaatca gactcggaac cgatgtgtgc tttaggggaat	2084			
190	Pro				
191	575				
193	tttaagttgc atgcatttca gagactttta gtcagttggt ttttattagc tgcttggtat	2144			
195	gcagtaactt ggggtggaggc aaaacactaa taaaagggct aaaaaggaaa atgatgcttt	2204			
197	tcttctatat tcttactctg tacaaataaa gaagttgctt gttgtttcag aagtttaacc	2264			

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199 cegttgcttg ttctgcagcc ctgtctactt gggcaccccc accacctggt agctgtgggt 2324
201 gtgcactgtc ttttgtagct ctggactgga ggggtagatg gggagtcaat taccatcac 2384
203 ataaatatga aacatttatc agaaatgttg ccattttaat gagatgattt tcttcatttc 2444
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212 <212> TYPE: PRT
213 <213> ORGANISM: Homo sapiens
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218 1 5 10 15
221 Gly Asp Arg Asp Pro Leu Pro Pro Gly Trp Glu Ile Lys Ile Asp Pro
222 20 25 30
225 Gln Thr Gly Trp Pro Phe Phe Val Asp His Asn Ser Arg Thr Thr Thr
226 35 40 45
229 Trp Asn Asp Pro Arg Val Pro Ser Glu Gly Pro Lys Glu Thr Pro Ser
230 50 55 60
233 Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser Arg Leu Pro Pro Ala Arg
234 65 70 75 80
237 Glu Gly His Pro Val Tyr Pro Gln Leu Arg Pro Gly Tyr Ile Pro Ile
238 85 90 95
241 Pro Val Leu His Glu Gly Ala Glu Asn Arg Gln Val His Pro Phe His
242 100 105 110
245 Val Tyr Pro Gln Pro Gly Met Gln Arg Phe Arg Thr Glu Ala Ala Ala
246 115 120 125
249 Ala Ala Pro Gln Arg Ser Gln Ser Pro Leu Arg Gly Met Pro Glu Thr
250 130 135 140
253 Thr Gln Pro Asp Lys Gln Cys Gly Gln Val Ala Ala Ala Ala Ala Ala
254 145 150 155 160
257 Gln Pro Pro Ala Ser His Gly Pro Glu Arg Ser Gln Ser Pro Ala Ala
258 165 170 175
261 Ser Asp Cys Ser Ser Ser Ser Ser Ala Ser Leu Pro Ser Ser Gly
262 180 185 190
265 Arg Ser Ser Leu Gly Ser His Gln Leu Pro Arg Gly Tyr Ile Ser Ile
266 195 200 205
269 Pro Val Ile His Glu Gln Asn Val Thr Arg Pro Ala Ala Gln Pro Ser
270 210 215 220
273 Phe His Gln Ala Gln Lys Thr His Tyr Pro Ala Gln Gln Gly Glu Tyr
274 225 230 235 240
277 Gln Thr His Gln Pro Val Tyr His Lys Ile Gln Gly Asp Asp Trp Glu
278 245 250 255
281 Pro Arg Pro Leu Arg Ala Ala Ser Pro Phe Arg Ser Ser Val Gln Gly
282 260 265 270
285 Ala Ser Ser Arg Glu Gly Ser Pro Ala Arg Ser Ser Thr Pro Leu His
286 275 280 285
289 Ser Pro Ser Pro Ile Arg Val His Thr Val Val Asp Arg Pro Gln Gln
290 290 295 300
293 Pro Met Thr His Arg Glu Thr Ala Pro Val Ser Gln Pro Glu Asn Lys

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294 305          310          315          320
297 Pro Glu Ser Lys Pro Gly Pro Val Gly Pro Glu Leu Pro Pro Gly His
298          325          330          335
301 Ile Pro Ile Gln Val Ile Arg Lys Glu Val Asp Ser Lys Pro Val Ser
302          340          345          350
305 Gln Lys Pro Pro Pro Pro Ser Glu Lys Val Glu Val Lys Val Pro Pro
306          355          360          365
309 Ala Pro Val Pro Cys Pro Pro Pro Ser Pro Gly Pro Ser Ala Val Pro
310          370          375          380
313 Ser Ser Pro Lys Ser Val Ala Thr Glu Glu Arg Ala Ala Pro Ser Thr
314 385          390          395          400
317 Ala Pro Ala Glu Ala Thr Pro Pro Lys Pro Gly Glu Ala Glu Ala Pro
318          405          410          415
321 Pro Lys His Pro Gly Val Leu Lys Val Glu Ala Ile Leu Glu Lys Val
322          420          425          430
325 Gln Gly Leu Glu Gln Ala Val Asp Asn Phe Glu Gly Lys Lys Thr Asp
326          435          440          445
329 Lys Lys Tyr Leu Met Ile Glu Tyr Leu Thr Lys Glu Leu Leu Ala
330          450          455          460
333 Leu Asp Ser Val Asp Pro Glu Gly Arg Ala Asp Val Arg Gln Ala Arg
334 465          470          475          480
337 Arg Asp Gly Val Arg Lys Val Gln Thr Ile Leu Glu Lys Leu Glu Gln
338          485          490          495
341 Lys Ala Ile Asp Val Pro Gly Gln Val Gln Val Tyr Glu Leu Gln Pro
342          500          505          510
345 Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln Ala Ile Met Glu Met Gly
346          515          520          525
349 Ala Val Ala Ala Asp Lys Gly Lys Lys Asn Ala Gly Asn Ala Glu Asp
350          530          535          540
353 Pro His Thr Glu Thr Gln Gln Pro Glu Ala Thr Ala Ala Ala Thr Ser
354 545          550          555          560
357 Asn Pro Ser Ser Met Thr Asp Thr Pro Gly Asn Pro Ala Ala Pro
358          565          570          575
361 <210> SEQ ID NO: 3
362 <211> LENGTH: 360
363 <212> TYPE: DNA
364 <213> ORGANISM: Homo sapiens
366 <220> FEATURE:
367 <221> NAME/KEY: misc_feature
368 <222> LOCATION: (1)..(360)
369 <223> OTHER INFORMATION: Specific sequence comprised inside BAG3 gene sequence
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377 atttccagac acttccacccc ctctctggcc acgtcacccc cgctttaat tcataaagggt      180
379 gcccggcgcc ggcttcccgg acacgtcgcc ggccgagagg ggcacacggc ggccggcccg      240
381 ccagagactc ggccggcgga gccagcgccc cgcacccgcg cccagcggg cagaccccaa      300
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/500,665

DATE: 07/14/2004
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Input Set : A:\PTO.FG.txt
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/500,665

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Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07142004\J500665.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date